

Amendments to the Claims

Claim 1 (currently amended): A method of performing a combined Chromatography and Mass Spectrometry analysis (C/MS) on at least one sample for the characterization of biomolecules species in the sample, which method comprises the steps of:

-performing an C/MS analysis(300);

-generating at least one first elution profile (305), ~~which said~~ first elution profile is being a multidimensional representation of the data resulting from the C/MS analysis wherein one dimension is an elution time of the chromatography, and one dimension is mass to charge ratio (m/z), and at least one dimension is a signal intensity, and in which of the elution profile a characteristic any variation in the signal intensity is an indication of the existence of a specific biomolecule species, and wherein the signal from each biomolecule species is dispersed forming a plurality of signal peaks associated with each biomolecule species in the elution profile; and

-reassembling the dispersed signal originating from one biomolecule species in the elution profile (310);

and ~~which method is characterized in that~~ further wherein said reassembling step ~~comprises~~ includes an automated annotation adapted to reassemble signal variations in the elution profile that originate from the same biomolecule species and generating a biomolecule map, said automated annotating being simultaneously based on at least both the elution time-dimension and the m/z-dimension.

Claim 2 (currently amended): The C/MS analysis method ~~according to~~ of claim 1, **wherein** the dispersion of signal from each biomolecule species arises from the

existence of different isotopes and/or charge states of the biomolecule species, and
wherein the automated ~~annotation species~~annotating reassembles the signal
dispersion for essentially each biomolecule caused by ~~both~~ the different isotopes
and/or different charge states of the biomolecule species.

Claim 3 (currently amended): The C/MS analysis method ~~according to~~of claim 2,
wherein the sample that comprises biomolecules species ~~has received~~includes
different chemical labels, ~~giving resulting in~~, at least, a first chemically labelled
biomolecule with a first label and a second mass-labelled biomolecule with a second
label, ~~the chemical difference~~said labels causing a further dispersion of the signal in
the elution profile, and wherein the automated annotation reassembles the signal
dispersion ~~inflicted~~caused by the chemical labelling.

Claim 4 (currently amended): The C/MS analysis method ~~according to~~of claim 3,
wherein the chemical labels are mass labels ~~giving resulting in~~ at least a first mass
labelled biomolecule with a first mass label and a second mass labelled biomolecule
with a second mass label, and wherein the mass difference causes a dispersion of the
signal in the elution profiles, and wherein the automated annotation reassembles the
signal dispersion inflicted by the mass labelling.

Claim 5 (currently amended): The C/MS analysis method ~~according to~~of claim 3,
wherein the chemical labels are isotope labels ~~giving resulting in~~ at least a first
isotope labelled biomolecule ~~comprising~~including isotopes of a first type and a
second isotope labelled biomolecule ~~comprising~~including isotopes of a second type,
the different isotopes causing a dispersion of the signal in the elution profiles, and

wherein the automated annotation reassembles the signal dispersion inflicted by the isotope labelling.

Claim 6 (currently amended): The C/MS analysis method of claim 2 according to any of claims 2 to 5, **wherein** the automated annotation in the reassembling of dispersed signals uses knowledge of the mass spectrometer resolution.

Claim 7 (currently amended): The C/MS analysis method according to of claim 6, **wherein** the automated annotation in the reassembling of dispersed signals uses a priori assumptions on the relations between different charge states and/or different isotopes of the same biomolecule species in the reassembling of dispersed signals.

Claim 8 (currently amended): The C/MS analysis method according to of claim 6, **wherein** the automated annotation in the reassembling of dispersed signals uses the an assumption that a first signal pattern associated with a first charge state of a biomolecule species has an resemblance with a second signal pattern associated with a second charge state of the biomolecule species.

Claim 9 (currently amended): The C/MS analysis method according to of claim 6, **wherein** the automated annotation in the reassembling of dispersed signals uses the an assumption that a first isotope distribution associated with a first charge state of a biomolecule species has an resemblance with a second isotope distribution associated with a second charge state of the biomolecule species.

Claim 10 (currently amended): The C/MS analysis method of claim 6 according to
any of claims 6 to 9, wherein the automated annotating comprises the steps of:

- a) *finding and marking* peaks in the signal variation of the first elution profile(310:1);
- b) *defining* a first set of spots, wherein each spot comprising-including at least one primary feature and said spots having have a variable extension in the m/z-dimension and a variable extension in the elution time dimension, and each spot is assumed to correspond at least to a specific charge state and an isotope or group of isotopes of a biomolecule (310:2);
- c) *constructing* a peptide map entry for each spot by detecting a set of regions with a known structural relationship and confining the patterns from one peptide species within the elution profile (310:3); and
- d) *repeating step-steps* (b) to (d) for each spot, and wherein, in the step of constructing a peptide map entry is created if for the charge state the structural relationships of the set of regions are essentially consistent and significant, and if no charge state giving essentially the known the structural relationships of the set of regions can be found, an incomplete peptide map entry is created from the spot itself.

Claim 11 (currently amended): The C/MS analysis method according toof claim 10,
wherein, the step of constructing a peptide entry comprises that, for each putative charge z , if possible, detecting additional isotopes at $m/z \pm 1/z$, $m/z \pm 2/z$, etc.
(310:3:1).

Claim 12 (currently amended): The C/MS analysis method according to or of claim 10,
wherein, the step of constructing a peptide entry comprises **that**, for each putative
charge z , ~~if possible~~, detecting additional charge states at $(m-1)/(z\pm 1)+1$, $(m-$
 $1)/(z\pm 2)+1$, etc. (310:3:2).

Claim 13 (currently amended): The C/MS analysis method according to or of claim 10,
wherein, the step of constructing a peptide entry comprises **that**, for each putative
charge z , ~~if possible~~, detecting different label variants, wherein the expected
displacement is specific for the labelling scheme used (310:3:3).

Claim 14 (currently amended): The C/MS analysis method according to or of claim 10,
wherein the step of constructing a peptide entry of the automated annotating
comprises at least two different modes reflecting the resolution characteristics of the
mass spectrometer.

Claim 15 (currently amended): The C/MS analysis method according to or of claim 14,
wherein the resolution of the spectrometer is dependent on m/z and described by a
spectrometer resolution parameter ($R(m/z)$), and the charge state assignment step
~~comprises~~ includes a high resolution mode and a low resolution mode, wherein the
shifting between the modes is dynamical, and the criteria for shifting between the
modes is dependent on m/z , z and the spectrometer resolution parameter.

Claim 16 (currently amended): The C/MS analysis method according to or of claim 15,
wherein for given m/z and z values the high resolution mode is used if:

$$\frac{m}{z} < \frac{1}{z} R\beta$$

wherein R spectrometer resolution parameter and β is an empirically predefined parameter, and
the low resolution mode is used otherwise.

Claim 17 (currently amended): The C/MS analysis method according to claim 1,
wherein the method further comprises the steps of:

-matching individual biomolecule maps (315) generated in the reassembling step (310), to form a global annotation;
-performing measurement and evaluation (320) for profiling the-a relative abundance of some of the individual biomolecule species across different samples, wherein the abundance profiles are based on the global annotation obtained in the preceding steps.

Claim 18 (currently amended): The C/MS analysis method according to claim 17,
wherein the method further comprises a step of defining subsets of biomolecule species (325), said step of defining subsets adapted for selecting subsets for further analysis, and the selection being based on variations in the-a relative abundance of some biomolecule species across different samples.

Claim 19 (currently amended): A measurement system for performing a combined Chromatography and Mass Spectrometry analysis (C/MS) on at least one sample for characterization of biomolecules species in the sample, wherein the measurement system comprises at least one chromatography column (125), a mass spectrometer interface (130), a mass spectrometer (135) and means for control and analysis (140,145), and the measurement system is adapted to:

-perform an C/MS analysis;

~~-generate~~ at least one first elution profile, ~~which~~ said first elution profile ~~is~~ being a multidimensional representations of the data resulting from the C/MS analysis wherein one dimension is an elution time of the chromatography, and one dimension is mass to charge ratio (m/z), and at least one dimension a signal intensity, and in which of the elution profile a characteristic any variation in the signal intensity is an indication of the existence of a specific biomolecule species, and wherein the signal from each biomolecule species is dispersed forming a plurality of signal peaks associated with each biomolecule species in the elution profile; and

~~-reassemble~~ the dispersed signal originating from one biomolecule species in the elution profile,

and ~~which~~ further wherein said measurement system is ~~characterized in that~~ reassembling ~~comprises~~ methodology ~~includes~~ an automated annotation adapted to reassemble signal variations in the elution profile that originate from the same biomolecule species and generating a biomolecule map, said automated annotating being simultaneously based on at least both the elution time-dimension and the m/z-dimension.

Claim 20 (currently amended): The measurement system ~~according to~~ of claim 19, further adapted to, in the automated annotation of dispersed signals, use knowledge of the mass spectrometer resolution for reassembling of signals originating from the same biomolecule species.

Claim 21 (currently amended): The measurement system ~~according to~~ of claim 20, **wherein** the automated annotating may operate in at least two different modes reflecting the resolution characteristics of the mass spectrometer.

Claim 22 (currently amended): The measurement system ~~according to~~^{of} claim 21, wherein the resolution of the spectrometer is dependent on m/z and described by a spectrometer resolution parameter (R(m/z)), and the charge state assignment step ~~comprises~~^{includes} a high resolution mode and a low resolution mode, wherein the shifting between the modes is dynamical, and the criteria for shifting between the modes is dependent on m/z, z and the spectrometer resolution parameter.

Claim 23 (currently amended): Computer program products directly loadable into the internal memory of a processing means within the means for controlling an analysing (140,145), comprising the software code means adapted for controlling the steps of ~~claim 1 any of the claims 1 to 18.~~

Claim 24 (currently amended): Computer program products stored on a computer usable medium, comprising readable program adapted for causing a processing means in a processing unit within the means for controlling an analysing (140,145), to control an execution of the steps of ~~claim 1 any of the claims 1 to 18.~~